



SEQUENCE LISTING

<110> Li, Zuomei
Bonfils, Claire
Besterman, Jeffrey

<120> Inhibition of Specific Histone Deacetylase Isoforms

<130> 106101.145

<140> US 09/817,913

<141> 2001-03-26

<150> US 60/192,157

<151> 2000-03-24

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 481

<212> PRT

<213> Human

<400> 1

Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
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Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
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His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
35 40 45

Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
50 55 60

Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
65 70 75 80

Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
85 90 95

Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
100 105 110

Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
 115 120 125

Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys
 130 135 140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
 145 150 155 160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
 165 170 175

Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg
 180 185 190

Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr
 195 200 205

Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val
 210 215 220

Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
 225 230 235 240

Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val
 245 250 255

Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
 260 265 270

Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
 275 280 285

Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr Ile
 290 295 300

Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
 305 310 315 320

Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
 325 330 335

Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln

340	345	350
Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn		
355	360	365
Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro		
370	375	380
Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro		
385	390	395
Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu		
405	410	415
Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys Asn		
420	425	430
Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys		
435	440	445
Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr		
450	455	460
Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu		
465	470	475
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<210> 2
 <211> 1611
 <212> DNA
 <213> Human

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 cgcagggcac ccggaggaaa gtctgttact actacgacgg ggatgttgga aattactatt 180
 atggacaagg ccaccaatg aagcctcacc gaatccgcac gactcataat ttgctgctca 240
 actatggtct ctaccgaaaa atggaaatct atcgccctca caaagccaat gctgaggaga 300
 tgaccaagta ccacagcgat gactacatta aattcttgcg ctccatccgt ccagataaca 360

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atggcctgtt tgagttctgt cagttgtcta ctggtggttc tgtggcaagt gctgtgaaac      480
ttaataagca gcagacggac atcgccgtga attgggctgg gggcctgcac catgcaaaga      540
agtccgaggc atctggcttc tgttacgtca atgatatcgt cttggccatc ctggaactgc      600
taaagtatca ccagaggggtg ctgtacattg acattgatat tcaccatggt gacggcgtgg      660
aagaggcctt ctacaccacg gaccgggtca tgactgtgtc ctttcataag tatggagagt      720
acttcccagg aactggggac ctacgggata ccggggctgg caaagacaag tattatgctg      780
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gtgtggaatt tgtcaagagc tttaacctgc ctatgctgat gctgggaggc ggtggttaca     1020
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aaaccaagga ggagaagcca gaagccaaag gggtaagga ggaggccaag ttggcctgaa     1560
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<210> 3
<211> 489
<212> PRT
<213> Human

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<400> 3
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Met Ala Tyr Ser Gln Gly Gly Gly Lys Lys Lys Cys Lys Val Cys Tyr
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Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro
20          25          30

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Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr
 35 40 45
 Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr Ala
 50 55 60
 Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu Arg
 65 70 75 80
 Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met His Ile
 85 90 95
 Pro Phe Asn Val Gly Glu Asp Cys Pro Ala Phe Asp Gly Leu Phe Glu
 100 105 110
 Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
 115 120 125
 Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
 130 135 140
 His Ala Lys Lys Tyr Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
 145 150 155 160
 Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
 165 170 175
 Ile Asp Ile Asp Ile His His Arg Gly Asp Gly Val Glu Glu Ala Phe
 180 185 190
 Tyr Thr Thr Asp Arg Val Met Thr Val Ser Phe Tyr Gly Glu Tyr Phe
 195 200 205
 Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr
 210 215 220
 Tyr Ala Val Asn Phe Pro Met Cys Asp Gly Ile Asp Asp Glu Ser Tyr
 225 230 235 240
 Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr Gln
 245 250 255

Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly Asp
 260 265 270

Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys Val
 275 280 285

Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly Gly
 290 295 300

Gly Tyr Thr Ile Leu Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr
 305 310 315 320

Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp
 325 330 335

Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser
 340 345 350

Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln
 355 360 365

Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln
 370 375 380

Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu
 385 390 395 400

Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys
 405 410 415

Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu
 420 425 430

Gly Gly Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Ala Arg Ile
 435 440 445

Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val Lys Glu
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Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr Lys Gly
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Thr Lys Ser Glu Gln Leu Ser Asn Pro

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 <211> 1985
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 cctcatagaa tccgcatgac ccataacttg ctgttaaatt atggcttaca cagaaaaatg 360
 gaaatatata ggccccataa agccactgcc gaagaaatga caaaatatca cagtgatgag 420
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 aaccagaaca ctccagaata tacggaaaag ataaaacagc gtttgtttga aaatttgcg 1320
 atgttacctc atgcacctgg tgtccagatg caagctattc cagaagatgc tgttcatgaa 1380
 gacagtggag atgaagatgg agaagatcca gacaagagaa tttctattcg agcatcagac 1440

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gaaacagagg acaaaaaaaaaac agacgttaag gaagaagata aatccaagga caacagtggg 1620
gaaaaaacag ataccaaagg aaccaaata gaacagctca gcaaccctg aatctgacag 1680
tctcaccaat ttcagaaaat cattaataag aaaatattga aaggaaaatg ttttcttttt 1740
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actttttcgt ttttgttttt ctgggcaagt tttattgtga gattttctaa ttatgaagca 1860
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<210> 5
<211> 428
<212> PRT
<213> Human

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<400> 5

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Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe
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His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
          20           25           30

```

```

His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
          35           40           45

```

```

Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
          50           55           60

```

```

Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
65           70           75           80

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```

Phe Thr Lys Ser Leu Asn Ala Pro Asn Val Gly Asp Asp Cys Pro Val
          85           90           95

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```

Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
          100          105          110

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Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Asn Trp
 115 120 125

Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe Cys
 130 135 140

Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Leu Lys Tyr
 145 150 155 160

His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
 165 170 175

Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe
 180 185 190

His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu
 195 200 205

Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg
 210 215 220

Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile
 225 230 235 240

Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys
 245 250 255

Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser
 260 265 270

Ile Arg Gly His Cys Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile
 275 280 285

Pro Pro Leu Leu Val Leu Gly Gly Gly Gly Tyr Thr Val Arg Asn Val
 290 295 300

Ala Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile
 305 310 315 320

Ser Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp
 325 330 335

Phe Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Ser Arg

340

345

350

Gln Tyr Leu Asp Gln Ile Arg Gln Thr Ile Phe Glu Asn Leu Lys Met
 355 360 365

Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu
 370 375 380

Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro
 385 390 395 400

Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly
 405 410 415

Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile
 420 425

<210> 6

<211> 1954

<212> DNA

<213> Human

<400> 6

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cctcactgac cgggtcatga cgggtgtcctt ccacaaatac ggaaattact tcttccttgg      660
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cctgcgggat ggcattgatg accagagtta caagcacctt ttccagccgg ttatcaacca      780
ggtagtggac ttctaccaac ccacgtgcat tgtgctccag tgtggagctg actctctggg      840

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<210> 7
 <211> 967
 <212> PRT
 <213> Human

<400> 7

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Met Leu Ala Met Lys His Gln Gln Glu Leu Leu Glu His Gln Arg Lys
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Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu Lys Gln His Arg Glu
          20           25           30

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```

Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys Gly Lys Glu Ser Ala
35           40           45

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Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln Glu Phe Val Leu Asn
50 55 60

Lys Lys Lys Ala Leu Ala His Pro Asn Leu Asn His Cys Ile Ser Ser
65 70 75 80

Cys Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His Ser Ser Leu Asp Gln
85 90 95

Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser Tyr Asn His Pro Val
100 105 110

Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro Leu Arg Lys Thr Ala
115 120 125

Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu Lys Gln Lys Val Ala
130 135 140

Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys Asp Gly Pro Val Val
145 150 155 160

Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr Asp Ser Ala Cys Ser
165 170 175

Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn Asn Ser Ser Gly Ser
180 185 190

Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val Pro Ser Ile Pro Ala
195 200 205

Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg Glu Gly Ser Ala Ala
210 215 220

Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro Asn Ile Thr Leu Gly
225 230 235 240

Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala Gly Gln Gln Asp Thr
245 250 255

Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg Leu Ser Leu Phe Pro
260 265 270

Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser Pro Leu Glu Arg Asp
 275 280 285

Gly Gly Ala Ala His Ser Pro Leu Leu Gln His Met Val Leu Leu Glu
 290 295 300

Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly Leu Gly Ala Leu Pro
 305 310 315 320

Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg Val Ser Pro Ser Ile
 325 330 335

His Lys Leu Arg Gln His Arg Pro Leu Gly Arg Thr Gln Ser Ala Pro
 340 345 350

Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu Val Ile Gln Gln Gln
 355 360 365

His Gln Gln Phe Leu Glu Lys His Lys Gln Gln Phe Gln Gln Gln Gln
 370 375 380

Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser Glu Pro Ala Arg Gln
 385 390 395 400

Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu Leu Arg Glu His Gln
 405 410 415

Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu Pro Gly Gln Lys Glu
 420 425 430

Ala His Ala Gln Ala Gly Val Gln Val Lys Gln Glu Pro Ile Glu Ser
 435 440 445

Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val Glu Pro Gly Gln Arg
 450 455 460

Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln Gln Ala Leu Leu Leu
 465 470 475 480

Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr Gln Ala Ser Met Glu
 485 490 495

Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His Arg Pro Leu Ser Arg

500					505					510					
Ala	Gln	Ser	Ser	Pro	Ala	Ser	Ala	Thr	Phe	Pro	Val	Ser	Val	Gln	Glu
	515					520						525			
Pro	Pro	Thr	Lys	Pro	Arg	Phe	Thr	Thr	Gly	Leu	Val	Tyr	Asp	Thr	Leu
	530					535					540				
Met	Leu	Lys	His	Gln	Cys	Thr	Cys	Gly	Ser	Ser	Ser	Ser	His	Pro	Glu
545					550					555					560
His	Ala	Gly	Arg	Ile	Gln	Ser	Ile	Trp	Ser	Arg	Leu	Gln	Glu	Thr	Gly
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Leu	Arg	Gly	Lys	Cys	Glu	Cys	Ile	Arg	Gly	Arg	Lys	Ala	Thr	Leu	Glu
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Glu	Leu	Gln	Thr	Val	His	Ser	Glu	Ala	His	Thr	Leu	Leu	Tyr	Gly	Thr
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Ser	Asp	Thr	Ile	Trp	Asn	Glu	Val	His	Ser	Ala	Gly	Ala	Ala	Arg	Leu
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Ala	Lys	Leu	Leu	Gln	Gln	Arg	Leu	Ser	Val	Ser	Lys	Ile	Leu	Ile	Val
705					710					715					720
Asp	Trp	Asp	Val	His	His	Gly	Asn	Gly	Thr	Gln	Gln	Ala	Phe	Tyr	Ser
				725					730					735	

Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg Tyr Asp Asp Gly Asn
 740 745 750

Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val Gly Thr Gly Pro Gly
 755 760 765

Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly Gly Leu Asp Pro Pro
 770 775 780

Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg Thr Val Val Met Pro
 785 790 795 800

Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu Ala Ser Ser Gly Phe
 805 810 815

Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly Gly Tyr Asn Leu Ser
 820 825 830

Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu Met Gly Leu Ala Gly
 835 840 845

Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His Asp Leu Thr Ala Ile
 850 855 860

Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu Leu Gly Asn Glu Leu
 865 870 875 880

Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg Pro Asn Ala Asn Ala
 885 890 895

Val Arg Ser Met Glu Lys Val Met Glu Ile His Ser Lys Tyr Trp Arg
 900 905 910

Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg Ser Leu Ile Glu Ala
 915 920 925

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 Cys Ser Ser Pro Asn Asp Ser Glu His Gly Pro Asn Pro Ile Leu Gly
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Page 35

Val Leu Ser Ser Ser Glu Thr Pro Ala Arg Thr Leu Pro Phe Leu Thr
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Gly Leu Ile Tyr Asp Ser Val Met Leu Lys His Gln Cys Ser Cys Gly
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Asp Asn Ser Arg His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp
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gactcctggg tgccatagagt gccaggggct gacaaagaag aagtggagga agtgaccgca 2880
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gaggaagaac ctatgaatct ctaaggctct ggaaccatct gcccgccac catgcccttg 3000
ggacctgggt ctcttctaac ccctggcaat agccccatt cctgggtctt tagagatcct 3060
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<210> 15
 <211> 377
 <212> PRT
 <213> Human

<400> 15

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Val Tyr Ile Tyr Ser Pro Glu Tyr Val Ser Met Cys Asp Ser Leu Ala
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Lys Ile Pro Lys Arg Ala Ser Met Val His Ser Leu Ile Glu Ala Tyr
 35 40 45
 Ala Leu His Lys Gln Met Arg Ile Val Lys Pro Lys Val Ala Ser Met
 50 55 60
 Glu Glu Met Ala Thr Phe His Thr Asp Ala Tyr Leu Gln His Leu Gln
 65 70 75 80
 Lys Val Ser Gln Glu Gly Asp Asp Asp His Pro Asp Ser Ile Glu Tyr
 85 90 95
 Gly Leu Gly Tyr Asp Cys Pro Ala Thr Glu Gly Ile Phe Asp Tyr Ala
 100 105 110
 Ala Ala Ile Gly Gly Ala Thr Ile Thr Ala Ala Gln Cys Leu Ile Asp
 115 120 125
 Gly Met Cys Lys Val Ala Ile Asn Trp Ser Gly Gly Trp His His Ala
 130 135 140
 Lys Lys Asp Glu Ala Ser Gly Phe Cys Tyr Leu Asn Asp Ala Val Leu
 145 150 155 160
 Gly Ile Leu Arg Leu Arg Arg Lys Phe Glu Arg Ile Leu Tyr Val Asp
 165 170 175
 Leu Asp Leu His His Gly Asp Gly Val Glu Asp Ala Phe Ser Phe Thr
 180 185 190
 Ser Lys Val Met Thr Val Ser Leu His Lys Phe Ser Pro Gly Phe Phe
 195 200 205
 Pro Gly Thr Gly Asp Val Ser Asp Val Gly Leu Gly Lys Gly Arg Tyr
 210 215 220
 Tyr Ser Val Asn Val Pro Ile Gln Asp Gly Ile Gln Asp Glu Lys Tyr
 225 230 235 240
 Tyr Gln Ile Cys Glu Ser Val Leu Lys Glu Val Tyr Gln Ala Phe Asn
 245 250 255

Pro Lys Ala Val Val Leu Gln Leu Gly Ala Asp Thr Ile Ala Gly Asp
 260 265 270

Pro Met Cys Ser Phe Asn Met Thr Pro Val Gly Ile Gly Lys Cys Leu
 275 280 285

Lys Tyr Ile Leu Gln Trp Gln Leu Ala Thr Leu Ile Leu Gly Gly Gly
 290 295 300

Gly Tyr Asn Leu Ala Asn Thr Ala Arg Cys Trp Thr Tyr Leu Thr Gly
 305 310 315 320

Val Ile Leu Gly Lys Thr Leu Ser Ser Glu Ile Pro Asp Asx Glu Phe
 325 330 335

Phe Thr Ala Tyr Gly Pro Asp Tyr Val Leu Glu Ile Thr Pro Ser Cys
 340 345 350

Arg Pro Asp Arg Asn Glu Pro His Arg Ile Gln Gln Ile Leu Asn Tyr
 355 360 365

Ile Lys Gly Asn Leu Lys His Val Val
 370 375

<210> 16
 <211> 1654
 <212> DNA
 <213> Human
 <220>
 <221> misc feature
 <222> (1590)..(1641)
 <223> Nucleotides 1590, 1592, 1600, 1607, 1611, 1630 and 1641 are "n" w
 herein "n" = any nucleotide.

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 cgagtatgtc agtatgtgtg actccctggc caagatcccc aaacggggcca gtatggtgca 180
 ttctttgatt gaagcatatg cactgcataa gcaaatgagg atagttaagc ctaaagtggc 240
 ctccatggag gagatggcca ccttccacac tgatgcttat ctgcagcatc tccagaaggt 300
 cagccaagag ggcatgatg atcatccgga ctccatagaa tatgggctag gttatgactg 360

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cccagccact gaagggatat ttgactatgc agcagctata ggaggggcta cgatcacagc 420
tgcccaatgc ctgattgacg gaatgtgcaa agtagcaatc aactgggtctg gaggggtggca 480
tcatgcaaag aaagatgaag catctggttt tcgttatctc aatgatgctg tcctgggaat 540
attacgattg cgacggaaat ttgagcgtat tccctacgtg gattcggatc tgcaccatgg 600
agatgggtga gaagacgcat tcagtttcac ctccaaagtc atgaccgtgt ccctgcacaa 660
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cctagggaaa acactatcct ctgagatccc agatcatgag tttttcacag catatggtcc 1080
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caaggggcat caagtggcag ctggcttcct ggggtgaaga ggcaggcacc ccagagtcct 1380
caactggacc taggggaaga aggagatarc ccacatttaa agttcttatt taaaaaaca 1440
cacacacaca aatgaaattt ttaatctttg aaaattattt ttaagcgaat tggggagggg 1500
agtattttta tcatcttaaa tgaaacagat cagaagctgg atgagagcag tcaccagttt 1560
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<210> 17
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<212> DNA
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<210> 18

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<211> 20
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<210> 19
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<210> 23
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<400> 23
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<210> 24
<211> 20
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<400> 24
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<400> 26
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<400> 28
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<400> 29

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<210> 31
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<400> 31
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<210> 32
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<400> 32
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<211> 20
<212> DNA
<213> Human

<400> 33
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